

> O < Intelligenetics  
> O < FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file 09-784340-1-q9r110.res made by jdelaval on Sun 2 Sep 101 10:45:02-PDT.

Query sequence being compared:US-09-784-340-1 (1-2759)  
Number of sequences searched: 1  
Number of scores above cutoff: 1

Results of the initial comparison of US-09-784-340-1 (1-2759) with:  
File : q9r110.pep

100-  
N -  
U 50-  
M -  
B -  
E -  
R -  
O -  
F 10-  
S -  
E 5-  
Q -  
U -  
N -  
E -  
C -  
S 0-  
SCORE 0 1 2 3 4 5 6 7 8 9  
SIDEV

PARAMETERS

Similarity matrix Unitary K-tuple 2  
Translation Frame 6  
Mismatch penalty 1 Joining penalty 20  
Gap penalty 1.00 Window size 32  
Gap size penalty 0.05  
Cutoff score 1  
Randomization group 0

SEARCH STATISTICS

Scores: Mean 9 Median 0 Standard Deviation 0.00  
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00  
Number of residues: 530  
Number of sequences searched: 1  
Number of scores above cutoff: 1

The scores below are sorted by initial score.  
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt.	Stg.	Frame
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1. q9r110	UDP GLUCURONOSYLTRANSFERASE U	530	9	81	0.00	1
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1. US-09-784-340-1 (1-2759)  
q9r110 UDP GLUCURONOSYLTRANSFERASE UGT2A3.

TOIG of: q9r110 check: 732 from: 1 to: 530

ID Q9R110 PRELIMINARY; PRT; 530 AA.  
AC Q9R110;  
DT 01-MAY-2000 (TEMBREL. 13, Created)  
DT 01-MAY-2000 (TEMBREL. 13, Last sequence update)  
DT 01-MAR-2001 (TEMBREL. 16, Last annotation update)  
DE UDP GLUCURONOSYLTRANSFERASE UGT2A3.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavillidae; Cavia.  
OX NCBI\_Taxid=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HARTLEY; TISSUE=LIVER;  
RA Smith S.A., Nagalla S.R., Andrews D.P., Olsen G.D.;  
RT "Morphine regulation of a novel uridine diphosphate  
glucuronosyltransferase in guinea pig pups following in utero  
RT exposure.";  
RL Mol. Genet. Metab. 0:0-0(1999).  
DR EMBL; AF175221; AAD51732.1; -  
DR InterPro; IPR002213; -  
DR Pfam; PF00201; UDPGT; 1.  
DR PROSITE; PS00375; UDPGT; 1.  
KW Transferase.  
SQ SEQUENCE 530 AA; 59895 MW; EE2E39AD3FD484E1 CRC64;

Q9R110 Length: 530 September 1, 2001 09:56 Type: P Check: 732 ..

Initial Score = 9 Optimized Score = 81 Significance = 0.00  
Residue Identity = 17% Matches = 108 Mismatches = 370  
Gaps = 133 Conservative Substitutions = 0  
Translation Frame= 1

QPIQISVGNCHHEVXQVFSISAPALLCWLMIMESPGVAILKHEPLAQGSHRSRHPXGNSIDSLK  
MAPGKLASAVILLILCCAGS-GFCGKYLWPC  
X  
80 90 100 110 120 130 140 150  
AFVNLQAFICIE--IXGPRATGONRRKXNICXPSSCLARLINLAISYIKKFFCCKRNF-KNDYXELX  
EMSHWLKLTLLLELVKRGHEVT-----VLTLSNLFIDYRHPAF-----NFEVLPYDVK  
40 50 60 70 80  
150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350  
LQSDAYEATGNOLRCNA--YRPGDSLMPDGYACSPFCAHT--XNFCR-----ROYGALMETSSSTFLC  
NMS---ENILNEFTIELAVNVPMPPLW-QSGKLLQOFFVOITEDLGLNCNNTYVNSLMLKRLDSKYDVLV  
90 100 110 120 130 140 150  
T-----CAVDRTRNONDLSGSKSKFNAISFPPLDLSGLRLSFLGRVLAAXGIRKKAHYIMXDCGSKXDMANTNI  
TDPVILPGELVAEMIGVPEVNLKFSMGHTIEKYCGQLPAPPSYVVPVLG--GLTTRMTFMERVKNNMFSLV  
160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350  
LGFXTSSTIIPYKLAVCMRIALXTCOSFAXGNGK-----PCPEPGRGRYCCGVFSYTVSKYRRKGXHX  
FDFTIOQDYKRFMDQFYSSEALGRPTTLCIEINGKAEIWLIRTYWDEF--PRPYLNFERY-----GGIHX  
230 240 250 260 270 280





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FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file 09-784340-1-q9r110.res made by jdelaval on Sun 2 Sep 101 10:45:46-PDT.

Query sequence being compared: US-09-784-340-1 (1-2759)  
Number of sequences searched: 1  
Number of scores above cutoff: 1

Results of the initial comparison of US-09-784-340-1 (1-2759) with:  
File: q9r110.pep

100-  
N -  
U 50-  
M -  
B -  
E -  
R -  
O -  
F 10-  
S -  
E 5-  
Q -  
U -  
E -  
N -  
C -  
E -  
S -  
0 -  
SCORE 0 1 2 3 4 5 6 7  
STDDEV

## PARAMETERS

Similarity matrix Unitary k-tuple 2  
Translation Frame 6  
Mismatch penalty 1 Joining penalty 20  
Gap penalty 1.00 Window size 32  
Gap size penalty 0.05  
Cutoff score 1  
Randomization group 0

## SEARCH STATISTICS

Scores: Mean Median Standard Deviation  
7 0 0.00  
Times: CPU Total Elapsed  
00:00:00.00 00:00:00.00

Number of residues: 530  
Number of sequences searched: 1  
Number of scores above cutoff: 1

The scores below are sorted by initial score.  
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Int. Opt.	Sign.	Frame
1. q9r110	UDP GLUCURONOSYLTRANSFERASE U	530	7	85	0.00	3

1. US-09-784-340-1 (1-2759)  
q9r110 UDP GLUCURONOSYLTRANSFERASE UGT2A3.

TOIG of: q9r110 check: 732 from: 1 to: 530

ID 09r110 PRELIMINARY; PRT; 530 AA.  
AC 09r110;  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
DE UDP GLUCURONOSYLTRANSFERASE UGT2A3.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HARTLEY; TISSUE=LIVER;  
RA Smith S.A., Nagalia S.R., Andrews D.P., Olsen G.D.;  
RT "Morphine regulation of a novel uridine diphosphate  
glucuronosyltransferase in guinea pig pups following in utero  
RT exposure.";  
RL Mol. Genet. Metab. 0:0-0(1999).  
DR EMBL; AF175221; AAD51732.1;  
DR InterPro; IPR002213;  
DR Pfam; PF00201; UDPGT; 1.  
DR PROSITE; PS00375; UDPGT; 1.  
KW Transferase.  
SQ SEQUENCE 530 AA; 59895 MW; E2F394D3FD484E1 CRC64;

09r110 Length: 530 September 1, 2001 09:56 Type: P Check: 732

Initial Score = 7 Optimized Score = 85 Significance = 0.00  
Residue Identity = 18% Matches = 112 Mismatches = 363  
Gaps = 134 Conservative Substitutions = 0  
Translation Frame = 3

TIADQCVRELPSXGLTSLQWYFCSSSVLAVDYSGKSWCGPVTYAIGIMRSFYKSSXXEMRXOYXLTOS  
10 20 30 40 50 60 70  
80 90 100 110 120 130 140  
LRLTGTSLHXLNLRMSICHRTEOKRMKYLTLXLMSCAAYOPGQNLKXMIFFLKXELKXCVBALSTIR  
150 160 170 180 190 200 210  
RLKRSYRKPTMKCLXTLFPVETXWLSCLQSLSLHLEFLKALWSEAVGNFQHPNYLCLXODXOTEXP  
120 130 140 150 160 170 180 190 200 210  
220 230 240 250 260 270 280  
FMKEKKIQCFQFCSTSGFRITITIFGKSEIVRHXE--GPLHYVRIMKIRGYXHYHIGILNLTNTLS-  
--ASAVALLLCCAGSGF-----CGK-VLVMPCEKSHMLNLTLEELVKGHE-----VTVALTSLN  
10 20 30 40 50 60  
290 300 310 320 330 340  
-LLED-----CTVNLPRKLCRLKWKILSRVQGMVLCWFCFHKMLQKRLIS--LLO-----PLPRSH  
NLFIDYNRPAFNEFVIVPPTDKNMS-----ENILNFIELAVNAVMPMLQSGKILQDFVOITEDGLNC  
70 80 90 100 110 120  
350 360 370 380 390 400  
R-RCYGGTKEKNHPIHXEPILGCMIGYPRMIFLYIPKPKLLSLM-VEKXGSMKLFITMG-----SLIMWEPY  
RNTVYVQSLMK-----KLKDSKYDVLVTDPIVPCGELVAEMLGVPFVNMKLFSGHTEIKYCGQLPAPPS

130	140	150	160	170	180	190
410	420	430	440	450	460	470
LVIISLTJLXJTR--	PKEOJXKXTSKLOAKIYXJLXBSQSEIPIPIKIMLXDYOFTMINIXSPXIEOSSGSS					
UVPVPLGJLTTBMTFEMERVKNNVFLVDFGFWI-----	QOYDKFMDOFYSALGRPTTLCEIMGKAEI					
200	210	220	230	240	250	
480	490	500	510	520	530	
SLSGATKEPSTCDOLPMTSPGSSSTJLMXJGSCXPMOL-----	LYSCSONVFYF-----	PVKNLIKTER				
WL-----	IRTYWDEEPFRPYLPNPEFVGJLHCKRAKLPKEMEEFVOSGSDGVVYSLSGSMXKNL--	TFEE				
260	270	280	290	300	310	320
540	550	560	570	580	590	600
XKRGNSFOJQERRPGVILILIPATJXNLVKTLLFSYLLPCYFIILAIXPRIPIXSGCEYISFRCJIFJVLTLF						
KANLIASALAQ--IPQKV--	JMYRKKKKRATIGCPNTRLF-----	DMIPONDILGHKTKTAFTIHHGSSNGCI				
330	340	350	360	370	380	
610	620	630	640	650	660	
SHFVQNGHEHYIXIFLFLISLFP-----	XNHYFSNLKXXDXDLQYADSWCJLHKHMDYKXXKMXNSQNS					
YBAIYHGVPMVGMPIF--	SDQPDNLGAKKAGAAVEVMNNTTSADLLGA---	LRIVINDPTIKENAMKLS				
390	400	410	420	430	440	
670	680	690	700	710	720	730
VNHTNOXSLIXHXLVMSNMJLFOFKXA--	LHHTQHYXSQTMNCKXKRXGJTLRIYVISTYILIXMSXPFE					
RHHND--	FVKFLDRAAFWEVEVMHNGKAKHLRYAANDLSMFQYHSLSVYIGFL--	ACVASAILLVTKCSLE				
450	460	470	480	490	500	510
740	750	760	770	780	790	800
LPBLSNHFICVLDDKXTVLILVKKKKKIKFSEYIEKMSIRSSXDYDFEISNHKKYUIVISDFIKFXLIVHL						
-SPONFIKIGRIKKE						
520	530					
810	820	830	840	850	860	870
IXMSILXNDNEYXPLFLSKXVAFVEKKKXADACESKSKKKKKKNTVMPRLBSVSLTAHCHAVTXYHIYDSPTVMLE						
880	890	900	910			
RSVSLTALSCVTSVSLTALSCVYVAIRKXOONTVSVIYA						

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Release 5.4

Results file 09-784340-1-q9r110.res made by jdelaval on Sun 2 Sep 10 10:46:00-PDT.

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query sequence being compared:US-09-784-340-1 (1-2759)
Number of sequences searched: 1
Number of scores above cutoff: 1

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Results of the initial comparison of US-09-784-340-1 (1-2759) with:  
File : q9r110.pep

Subject	Score
N	100
U	95
M	90
B	85
E	80
R	75
O	70
F	65
S	60
E	55
Q	50
D	45
N	40
C	35
E	30

## PARAMETERS

	Unary	K-tuple
Similarity matrix	6	20
Translation frame	1	32
Mismatch penalty	1.00	
Gap penalty	0.05	
Gap size penalty		
Cutoff score	0.01	
Randomization group	0	

## SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	7	0	0.00
Times:	CPU		Total Elapsed
	00:00:00.00		00:00:00.00
Number of residues:		530	
Number of sequences searched:		1	
Number of scores above cutoff:		1	

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found

The list of best scores is:

Sequence Name	Description	Length	Score	Opt.	Sig.	Frame
1. q9r110	UDP GLUCURONOSYLTRANSFERASE U	530	7	82	0.00	4

1. US-09-784-340-1 (1-2759)  
q9r110 UDP GLUCURONOSYLTRANSFERASE UGT2A3.

TOIG of: q9r110 check: 732 from: 1 to: 530

ID Q9r110 PRELIMINARY: PRT: 530 AA.  
AC Q9r110:  
DT 01-MAY-2000 (TREMBLER, 13, Created)  
DT 01-MAY-2000 (TREMBLER, 13, Last sequence update)  
DE 01-MAR-2001 (TREMBLER, 16, Last annotation update)  
DE UDP GLUCURONOSYLTRANSFERASE UGT2A3.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognath; Cavidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=HARTLEY; TISSUE=LIVER;  
RA Smith S.A., Nagalla S.R., Andrews D.P., Olsen G.D.;  
RT Morphine regulation of a novel uridine diphosphate  
RT glucuronosyltransferase in guinea pig pups following in utero  
RT exposure;  
RL Mol. Genet. Metab. 0:0-0(1999).  
DR EMBL: AF175221; AAD51732.1; -;  
DR InterPro: IPR002213; -;  
DR Pfam: PF00201; UDPGT; 1.  
DR PROSITE: PS00375; UDPGT; 1.  
KW Transferase.  
SQ SEQUENCE 530 AA: 59895 MW: EE2F394D3FD484E1 CRC64;

Q9r110 length: 530 September 1, 2001 09:56 Type: P Check: 732 ..

Initial Score = 7 Optimized score = 82 Significance = 0.00  
Residue Identity = 184 Matches = 109 Mismatches = 354  
Gaps = 134 Conservative Substitutions = 0  
Translation Frame= 4

RYVADVSLSTIRVFAKCCORARNAKCCORATXRHDSVAVNDMLRNGMTVGCQRATXRHDSVFF  
80 90 100 110 120 130 140  
FFFTPTSTISLEFYKSLYFLXKRLXLYFIILKNRHLNQVYYOLKFKIRNMYNHIIFLWVYLLKILCLTXISY  
150 160 170 180 190 200 210  
GHFLYVRKFOFLLEFDNNKNCLEFLIKNTOKSVAKWCKRLXHLDEVCNINANYSECNALSSFLAITHCLRS  
X  
MAPGKLAS

220 230 240 250 260 270 280  
VNLGKMGKGLFKLTKKNNHYTHNKL-----MSXNASLICVYVXILKILHFLLLYH-VFVOT--PGISILQVT  
AVL-----LLILCCAGSGCGKVLVWPCMSHMLN-----KTLLEELVKGHEVTVLLSNLFLTDYNR  
10 20 30 40 50 60  
290 300 310 320 330 340  
LSLKVREVTSMKQYOKXENLDVMSLCHKY--REESHKTXENATKEDILTTSXWNSR---LYGSKD-  
HPAFNFEVIVPPTDKMSENILNEFIELAVNVPWPTWQSKLLQGFVQTTEDLGLNCRRTVYNQSLMKK  
70 80 90 100 110 120 130 140

350 360 370 380 390 400  
ITXIIKKKXGFOHILCGNNKODYIRSLFLN-LERS-----IPSLFEXFYXIFDRKIRNIIATRI  
LRDSKYDVLTVDPIPCGELVAMGLVFPVNMILKFSMGHTIEKYGQLPAPPS-----YVPVPLGGLTTRM

150 160 170 180 190 200  
410 420 430 440 450 460 470  
XOLPHRSAGTOSHLSXSGTRXGHHGOLLAGWMLLCGAXQTSRRLDLGALQYDNG--EFLISXHSLYKRN  
TIPHERKNNWFSYL-----FDFWIOQYDKFW-----DOFYSALGRPTTLEINGKRAIWIIRTYWDEEP  
210 220 230 240 250 260  
480 490 500 510 520 530  
RXKLFSKPSV-NLRLSXFXSL-----FLQ-----LLIMPSCELCYQADHQIMWLPXPXGPHKXLR  
RPVLPNFEFVGGHCKPAKPLPKEMEEFVQSGEDGVVVFSGSMWKNTTEKANKLASALQIP-QKVLNR  
270 280 290 300 310 320 330  
540 550 560 570 580 590  
-----SHSFHHEXKLMFWDDQEDHSVSNHTAELWLMWVFLCTSTPVSQSGGOLKQXYPFLXHFET  
YKGRKPATLGPNTFLFDMIPQNDLGHPTKA-----FIT-HGSSNGIYEATY-----  
340 350 360 370 380 390  
600 610 620 630 640 650 660  
VTPEKTPQYHPLMSGO--NPFEPXAKIMQV-----YSAIIQOTQSYGVNBEIQNPMMFVLAISQLEPQ  
--HGVPVWGPITFSDQPDNLGKAKAGAVEVNMNTSADLIGALRTVINPTYKENAMKLSRIHHDQPV  
390 400 410 420 430 440 450  
670 680 690 700 710 720  
SHIMXWAF-----LMYYKTL--PKNDSRNPESSRSGTKLALNLFLEPERSFCLVLSXAQYHRRKVEVS  
KPLDRAATWVEFVNHKAKKILRYAANHLMSWFOYS--LDVIGFLACVASAILLV-----TKCLPFSF  
460 470 480 490 500 510  
730 740 750 760 770 780 790  
HSFAFYCLKQKFXVXAKQGLQATOPSGLHRESQGLXALHRSWFPVASSXASDCXSSHTSTLKNLTPQOKNH  
ONFIKIKRIKKE  
520 530  
800 810 820 830 840 850 860  
LILXILARLISLARHSELGQITFHFLLCPVAVYPPPOISMOKASQSLTKALSESILLPHGLSLXALLEXPX  
870 880 890 900 910  
HANGSCHNATGGLSHRHSQHRRAAGAEIPKLTQTSXWCPPTLIGN

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FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file 09-784340-1-q9r110.res made by jdelaval on Sun 2 Sep 101 10:46:10-PDT.

Query sequence being compared:US-09-784-340-1 (1-2759)  
Number of sequences searched: 1  
Number of scores above cutoff: 1

Results of the initial comparison of US-09-784-340-1 (1-2759) with:  
File : q9r110.pep

100-  
N -  
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F 10-  
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O 5-  
O -  
U -  
E -  
N -  
C -  
E -  
S 0-  
SCORE 0 1 1 2 2 3 3 4 4 5  
SIDEV

PARAMETERS

Similarity matrix Unitary k-tuple 2  
Translation Frame 6  
Mismatch penalty 1 Joining penalty 20  
Gap penalty 1.00 Window size 32  
Gap size penalty 0.05  
Cutoff score 1  
Randomization group 0

SEARCH STATISTICS

Scores: Mean 5 Median 0 Standard Deviation 0.00  
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00  
Number of residues: 530  
Number of sequences searched: 1  
Number of scores above cutoff: 1

The scores below are sorted by initial score.  
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt.	Seq. Frame
1. q9r110	UDP GLUCURONOSYLTRANSFERASE U	530	5	72	0.00 5

1. US-09-784-340-1 (1-2759)  
q9r110 UDP GLUCURONOSYLTRANSFERASE UGT2A3.

TOIG of: q9r110 check: 732 from: 1 to: 530

ID 09r110 PRELIMINARY; PRT; 530 AA.  
AC 09r110.  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
DE UDP GLUCURONOSYLTRANSFERASE UGT2A3.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HARTLEY; TISSUE=LIVER;  
RA Smith S.A., Nagalia S.R., Andrews D.P., Olsen G.D.;  
RT "Morphine regulation of a novel uridine diphosphate  
glucuronosyltransferase in guinea pig pups following in utero  
exposure.";  
RL Mol. Genet. Metab. 0:0-0(1999).  
DR EMBL; AF175221; AAD51732.1; -  
DR InterPro: IPR002213; -  
DR Pfam; PF00201; UDPGT; 1.  
DR PROSITE; PS00375; UDPGT; 1.  
KW Transferase.  
SQ SEQUENCE 530 AA; 59895 MW; EE2F394D3FD484E1 CRC64;

09r110 Length: 530 September 1, 2001 09:56 Type: P Check: 732 ..

Initial Score = 5 Optimized Score = 72 Significance = 0.00  
Residue Identity = 18% Matches = 92 Mismatches = 318  
Gaps = 101 Conservative Substitutions = 5  
Translation Frame= 5

ATXRLTVFCCORATYATXRHDSAVNDTLVTHDSAVNDTLRNGMTVSLTICVYTAQOMAVNDTLRNGMTVFFFF  
80 90 100 110 120 130 140  
FFLHSEQASLVESYVNFEDVRDKNVEYSSFRIDIXIKCTINKNFISEITFYFWMLLSKKSXVLEVLM  
150 160 170 180 190 200 210  
DIFSXMKNSEFFYILRTIIRFVYLSSTRHKKCOQSDGRNNGVDIMRYVEIXOTLLSWMPRIHFEKQPIVXQ  
220 230 240 250 260 270 280  
XCVWCRRAYLVNKKRIIMLLTSCXCHMLHXFWFTEPCEFIYFFTSKCLCKHQSAYCSPYHLRLKRX  
290 300 310 320 330 340 350  
XKHGNSDIRNRKRIKMYSCPCVTKKXKRVSTPRKORKNEIYSQPHDGIILGIIAKIKQNRKXENSKYFTKF  
360  
YVAGINRITPSGLSXIMWDLPLFLYLSFIFLTKGKKTKFCGEQYSSCHTQOQEPNHIYRVVLEPGEVWGSX  
370 380 390 400 410 420 430  
440 450 460 470 480 490 500  
SOVLGSFVAHDKLDPEDCSIXGLYRLIWNVSXSHSILFIRIGNDKCSQPOXIFPACHSFEVYFSCFGLH  
410 420 430 440 450 460 470 480 490 500  
MAPGLASAVL---LLILCCAGS---GFCGKVLWPCQENSHWL-  
510 520 530 540 550 560  
VSYVIRKLITKGNSHHRDPMV-----NSFTDPIHSTMSDKSFGFGTKR---TILGIYIIPSTIGSXCXG  
510 520 530 540 550 560  
-----NLKTLLEELVKGHEVYVLTLSNNLFLDYNRHAPFNEFVLPVPTDRNMSENILNEFI-----







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